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     (FILE 'HOME' ENTERED AT 14:22:42 ON 11 MAY 2007)

     FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 14:22:59 ON 11
     MAY 2007
L1            43 S (C MANNOSYLATE?)
L2             4 S L1 AND PROTEASE?
L3            42 S L1 AND PROTEIN?
L4        186739 S (FUSION PROTEIN)
L5             1 S L4 AND L1
L6             0 S L5 AND L2
L7             1 DUPLICATE REMOVE L2 (3 DUPLICATES REMOVED)

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L5 ANSWER 1 OF 1 MEDLINE on STN
AN 2002352948 MEDLINE
DN PubMed ID: 12096136
TI C-mannosylation and o-fucosylation of thrombospondin type 1 repeats.
AU Gonzalez de Peredo Anne; Klein Dominique; Macek Boris; Hess Daniel; Peter-Katalinic Jasna; Hofsteenge Jan
CS Friedrich Miescher Institute for Biomedical Research, Novartis Research Foundation, Maulbeerstrasse 66, CH-4058 Basel, Switzerland.
SO Molecular & cellular proteomics : MCP, (2002 Jan) Vol. 1, No. 1, pp. 11-8. Journal code: 101125647. ISSN: 1535-9476.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200208
ED Entered STN: 4 Jul 2002
Last Updated on STN: 14 Aug 2002
Entered Medline: 13 Aug 2002
AB The final chemical structure of a newly synthesized protein is often only attained after further covalent modification. Ideally, a comprehensive proteome analysis includes this aspect, a task that is complicated by our incomplete knowledge of the range of possible modifications and often by the lack of suitable analysis methods. Here we present two recently discovered, unusual forms of protein glycosylation, i.e. C-mannosylation and O-fucosylation. Their analysis by a combined mass spectrometric approach is illustrated with peptides from the thrombospondin type 1 repeats (TSRs) of the recombinant axonal guidance protein F-spondin. Nano-electrospray ionization tandem-mass spectrometry of isolated peptides showed that eight of ten Trp residues in the TSRs of F-spondin are C-mannosylated. O-Fucosylation sites were determined by a recently established nano-electrospray ionization quadrupole time-of-flight tandem-mass spectrometry approach. Four of five TSRs carry the disaccharide Hex-dHex-O-Ser/Thr in close proximity to the C-mannosylation sites. In analogy to thrombospondin-1, we assume this to be Glc-Fuc-O-Ser/Thr. Our current knowledge of these glycosylations will be discussed.
CT Amino Acid Motifs
*Fucose: ME, metabolism
*Glycopeptides: CH, chemistry
Glycosylation
*Growth Substances
Humans
*Mannose: ME, metabolism
*Mass Spectrometry: MT, methods
*Neural Cell Adhesion Molecules: ME, metabolism
*Peptides
Protein Processing, Post-Translational
Recombinant Fusion Proteins: CH, chemistry
Thrombospondin 1: CH, chemistry
*Thrombospondin 1: ME, metabolism
RN 31103-86-3 (Mannose); 3713-31-3 (Fucose)
CN 0 (Glycopeptides); 0 (Growth Substances); 0 (Neural Cell Adhesion Molecules); 0 (Peptides); 0 (Recombinant Fusion Proteins); 0 (SPON1 protein, human); 0 (Thrombospondin 1)

L5 ANSWER 1 OF 1 MEDLINE on STN
AN 2002352948 MEDLINE
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SO Molecular & cellular proteomics : MCP, (2002 Jan) Vol. 1, No. 1, pp. 11-8. Journal code: 101125647. ISSN: 1535-9476.
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LA English
FS Priority Journals
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Entered Medline: 13 Aug 2002
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CT Amino Acid Motifs
*Fucose: ME, metabolism
*Glycopeptides: CH, chemistry
Glycosylation
*Growth Substances
Humans
*Mannose: ME, metabolism
*Mass Spectrometry: MT, methods
*Neural Cell Adhesion Molecules: ME, metabolism
*Peptides
Protein Processing, Post-Translational
Recombinant Fusion Proteins: CH, chemistry
Thrombospondin 1: CH, chemistry
*Thrombospondin 1: ME, metabolism
RN 31103-86-3 (Mannose); 3713-31-3 (Fucose)
CN 0 (Glycopeptides); 0 (Growth Substances); 0 (Neural Cell Adhesion Molecules); 0 (Peptides); 0 (Recombinant Fusion Proteins); 0 (SPON1 protein, human); 0 (Thrombospondin 1)

ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
DUPLICATE 1
AN 1998:167870 BIOSIS
DN PREV199800167870
TI Protein C-mannosylation is enzyme-catalysed and uses dolichyl-phosphate-mannose as a precursor.
AU Doucey, Marie-Agnes; Hess, Daniel; Cacan, Rene; Hofsteenge, Jan [Reprint author]
CS Friedrich Miescher-Inst., PO Box 2543, CH-4002 Basel, Switzerland
SO Molecular Biology of the Cell, (Feb., 1998) Vol. 9, No. 2, pp. 291-300. print.
CODEN: MBCEEV. ISSN: 1059-1524.
DT Article
LA English
ED Entered STN: 6 Apr 1998
Last Updated on STN: 4 May 1998
AB C-mannosylation of Trp-7 in human ribonuclease 2 (RNase 2) is a novel kind of protein glycosylation that differs fundamentally from N- and O-glycosylation in the protein-sugar linkage. Previously, we established that the specificity determinant of the acceptor substrate (RNase 2) consists of the sequence W-x-x-W, where the first Trp becomes C-mannosylated. Here we investigated the reaction with respect to the mannosyl donor and the involvement of a glycosyltransferase. C-mannosylation of Trp-7 was reduced 10-fold in CHO (Chinese hamster ovary) Lec15 cells, which are deficient in dolichylphosphate-mannose (Dol-P-Man) synthase activity, compared with wild-type cells. This was not a result of a decrease in C-mannosyltransferase activity. Rat liver microsomes were used to C-mannosylate the N-terminal dodecapeptide from RNase 2 in vitro, with Dol-P-Man as the donor. This microsomal transferase activity was destroyed by heat and protease treatment, and displayed the same acceptor substrate specificity as the in vivo reaction studied previously. The C-C linkage between the indole and the mannosyl moiety was demonstrated by tandem electrospray mass spectrometry analysis of the product. GDP-Man, in the presence of Dol-P, functioned as a precursor in vitro with membranes from wild-type but not CHO Lec15 cells. In contrast, with Dol-P-Man both membrane preparations were equally active. It is concluded that a microsomal transferase catalyses C-mannosylation of Trp-7, and that the minimal biosynthetic pathway can be defined as: Man -> GDP-Man -> Dol-P-Man -> (C2-Man-)Trp.
CC Metabolism - Proteins, peptides and amino acids 13012
Enzymes - Physiological studies 10808
Digestive system - Physiology and biochemistry 14004
IT Major Concepts
Metabolism
IT Parts, Structures, & Systems of Organisms
liver microsome
IT Chemicals & Biochemicals
dolichyl-phosphate-mannose synthase; glycosyltransferase; microsomal transferase: activity; C-mannosyltransferase: activity
IT Miscellaneous Descriptors
protein C-mannosylation
ORGN Classifier
Cricetidae 86310
Super Taxa
Rodentia; Mammalia; Vertebrata; Chordata; Animalia
Organism Name
CHO Lec15
Taxa Notes
Animals, Chordates, Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Muridae 86375
Super Taxa
Rodentia; Mammalia; Vertebrata; Chordata; Animalia

Organism Name
rat
Taxa Notes
Animals, Chordates, Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

RN 62213-44-9 (dolichyl-phosphate-mannose synthase)
9033-07-2 (glycosyltransferase)
9047-61-4 (TRANSFERASE)

=>

10/530,457
L/COOK 5/11/07

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(FILE 'HOME' ENTERED AT 15:23:44 ON 11 MAY 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 15:30:31 ON 11 MAY 2007

```
L1            98 S (C MANNOSYLAT?)
L2             8 S (C MANNOSYLTRAN?)
L3             0 S L1 AND MODULAT?
L4             1 S L2 AND MODULAT?
L5             0 S L1 AND SCREEN?
L6             6 S L1 AND DRUG?
L7             5 DUPLICATE REMOVE L6 (1 DUPLICATE REMOVED)
L8             3 S L7 AND PD<2004
L9             5 S L1 AND GPI?
L10            0 S L8 AND L9
L11            5 S L9 AND PD<2004
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d his

     (FILE 'HOME' ENTERED AT 15:23:44 ON 11 MAY 2007)

     FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 15:30:31 ON 11
     MAY 2007
L1            98 S (C MANNOSYLAT?)
L2             8 S (C MANNOSYLTRAN?)
L3             0 S L1 AND MODULAT?
L4             1 S L2 AND MODULAT?
L5             0 S L1 AND SCREEN?
L6             6 S L1 AND DRUG?
L7             5 DUPLICATE REMOVE L6 (1 DUPLICATE REMOVED)
L8             3 S L7 AND PD<2004
L9             5 S L1 AND GPI?
L10            0 S L8 AND L9
L11            5 S L9 AND PD<2004

=>
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ANSWER 5 OF 5 MEDLINE on STN
AN 2002301128 MEDLINE
DN PubMed ID: 12042244
TI Protein glycosylation: nature, distribution, enzymatic formation, and disease implications of glycopeptide bonds.
AU Spiro Robert G
CS Department of Biological Chemistry, Harvard Medical School and the Joslin Diabetes Center, One Joslin Place, Boston, MA 02215, USA.
NC DK17325 (NIDDK)
DK17477 (NIDDK)
SO Glycobiology, (2002 Apr) Vol. 12, No. 4, pp. 43R-56R. Ref: 166
Journal code: 9104124. ISSN: 0959-6658.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 200211
ED Entered STN: 4 Jun 2002
Last Updated on STN: 14 Dec 2002
Entered Medline: 27 Nov 2002
AB Formation of the sugar-amino acid linkage is a crucial event in the biosynthesis of the carbohydrate units of glycoproteins. It sets into motion a complex series of posttranslational enzymatic steps that lead to the formation of a host of protein-bound oligosaccharides with diverse biological functions. These reactions occur throughout the entire phylogenetic spectrum, ranging from archaea and eubacteria to eukaryotes. It is the aim of this review to describe the glycopeptide linkages that have been found to date and specify their presence on well-characterized glycoproteins. A survey is also made of the enzymes involved in the formation of the various glycopeptide bonds as well as the site of their intracellular action and their affinity for particular peptide domains is evaluated. This examination indicates that 13 different monosaccharides and 8 amino acids are involved in glycoprotein linkages leading to a total of at least 41 bonds, if the anomeric configurations, the phosphoglycosyl linkages, as well as the GPI (glycophosphatidylinositol) phosphoethanolamine bridge are also considered. These bonds represent the products of N- and O-glycosylation, C-mannosylation, phosphoglycation, and glypiation. Currently at least 16 enzymes involved in their formation have been identified and in many cases cloned. Their intracellular site of action varies and includes the endoplasmic reticulum, Golgi apparatus, cytosol, and nucleus. With the exception of the Asn-linked carbohydrate and the GPI anchor, which are transferred to the polypeptide en bloc, the sugar-amino acid linkages are formed by the enzymatic transfer of an activated monosaccharide directly to the protein. This review also deals briefly with glycosidases, which are involved in physiologically important cleavages of glycopeptide bonds in higher organisms, and with a number of human disease states in which defects in enzymatic transfer of saccharides to protein have been implicated.
CT *Disease
*Glycopeptides: ME, metabolism
Glycosylation
Humans
Proteins: CH, chemistry
*Proteins: ME, metabolism
CN 0 (Glycopeptides); 0 (Proteins)

=>

ANSWER 5 OF 5 MEDLINE on STN
AN 2002301128 MEDLINE
DN PubMed ID: 12042244
TI Protein glycosylation: nature, distribution, enzymatic formation, and disease implications of glycopeptide bonds.
AU Spiro Robert G
CS Department of Biological Chemistry, Harvard Medical School and the Joslin Diabetes Center, One Joslin Place, Boston, MA 02215, USA.
NC DK17325 (NIDDK)
DK17477 (NIDDK)
SO Glycobiology, (2002 Apr) Vol. 12, No. 4, pp. 43R-56R. Ref: 166
Journal code: 9104124. ISSN: 0959-6658.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 200211
ED Entered STN: 4 Jun 2002
Last Updated on STN: 14 Dec 2002
Entered Medline: 27 Nov 2002
AB Formation of the sugar-amino acid linkage is a crucial event in the biosynthesis of the carbohydrate units of glycoproteins. It sets into motion a complex series of posttranslational enzymatic steps that lead to the formation of a host of protein-bound oligosaccharides with diverse biological functions. These reactions occur throughout the entire phylogenetic spectrum, ranging from archaea and eubacteria to eukaryotes. It is the aim of this review to describe the glycopeptide linkages that have been found to date and specify their presence on well-characterized glycoproteins. A survey is also made of the enzymes involved in the formation of the various glycopeptide bonds as well as the site of their intracellular action and their affinity for particular peptide domains is evaluated. This examination indicates that 13 different monosaccharides and 8 amino acids are involved in glycoprotein linkages leading to a total of at least 41 bonds, if the anomeric configurations, the phosphoglycosyl linkages, as well as the GPI (glycophosphatidylinositol) phosphoethanolamine bridge are also considered. These bonds represent the products of N- and O-glycosylation, C-mannosylation, phosphoglycation, and glypiation. Currently at least 16 enzymes involved in their formation have been identified and in many cases cloned. Their intracellular site of action varies and includes the endoplasmic reticulum, Golgi apparatus, cytosol, and nucleus. With the exception of the Asn-linked carbohydrate and the GPI anchor, which are transferred to the polypeptide en bloc, the sugar-amino acid linkages are formed by the enzymatic transfer of an activated monosaccharide directly to the protein. This review also deals briefly with glycosidases, which are involved in physiologically important cleavages of glycopeptide bonds in higher organisms, and with a number of human disease states in which defects in enzymatic transfer of saccharides to protein have been implicated.
CT *Disease
*Glycopeptides: ME, metabolism
Glycosylation
Humans
Proteins: CH, chemistry
*Proteins: ME, metabolism
CN 0 (Glycopeptides); 0 (Proteins)

=>

ANSWER 1 OF 3 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

AN 2001400853 EMBASE

TI Requirement of the Lec35 gene for all known classes of monosaccharide-P-dolichol-dependent glycosyltransferase reactions in mammals.

AU Anand M.; Rush J.S.; Ray S.; Doucey M.-A.; Weik J.; Ware F.E.; Hofsteenge J.; Waechter C.J.; Lehrman M.A.

CS M.A. Lehrman, Department of Pharmacology, UT-Southwestern Medical Center, Dallas, TX 75390-9041, United States. mlehrm@mednet.swmed.edu

SO Molecular Biology of the Cell, (2001) Vol. 12, No. 2, pp. 487-501. .
Refs: 47
ISSN: 1059-1524 CODEN: MBCEEV

CY United States

DT Journal; Article

FS 022 Human Genetics
029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 30 Nov 2001
Last Updated on STN: 30 Nov 2001

AB The Lec35 gene product (Lec35p) is required for utilization of the mannose donor mannose-P-dolichol (MPD) in synthesis of both lipid-linked oligosaccharides (LLOs) and glycosylphosphatidylinositols, which are important for functions such as protein folding and membrane anchoring, respectively. The hamster Lec35 gene is shown to encode the previously identified cDNA SL15, which corrects the Lec35 mutant phenotype and predicts a novel endoplasmic reticulum membrane protein. The mutant hamster alleles Lec35.1 and Lec35.2 are characterized, and the human Lec35 gene (mannose-P-dolichol utilization defect 1) was mapped to 17p12-13. To determine whether Lec35p was required only for MPD-dependent mannosylation of LLO and glycosylphosphatidylinositol intermediates, two additional lipid-mediated reactions were investigated: MPD-dependent C-mannosylation of tryptophanyl residues, and glucose-P-dolichol (GPD)-dependent glucosylation of LLO. Both were found to require Lec35p. In addition, the SL15-encoded protein was selective for MPD compared with GPD, suggesting that an additional GPD-selective Lec35 gene product remains to be identified. The predicted amino acid sequence of Lec35p does not suggest an obvious function or mechanism. By testing the water-soluble MPD analog mannose-β-1-P-citronellol in an in vitro system in which the MPD utilization defect was preserved by permeabilization with streptolysin-O, it was determined that Lec35p is not directly required for the enzymatic transfer of mannose from the donor to the acceptor substrate. These results show that Lec35p has an essential role for all known classes of monosaccharide-P-dolichol-dependent reactions in mammals. The in vitro data suggest that Lec35p controls an aspect of MPD orientation in the endoplasmic reticulum membrane that is crucial for its activity as a donor substrate.

CT Medical Descriptors:
*gene isolation
*carbohydrate analysis
*enzyme analysis
*enzyme mechanism
protein folding
hamster
phenotype
endoplasmic reticulum
gene mutation
amino acid sequence
catalysis
fluorescence in situ hybridization
mammal
nonhuman

ANSWER 1 OF 3 EMBASE

AN 2001400853 EMBASE

TI Requirement of the Lec35 gene for all known classes of monosaccharide-P-dolichol-dependent glycosyltransferase reactions in mammals.

AU Anand M.; Rush J.S.; Ray S.; Doucey M.-A.; Weik J.; Ware F.E.; Hofsteenge J.; Waechter C.J.; Lehrman M.A.

CS M.A. Lehrman, Department of Pharmacology, UT-Southwestern Medical Center, Dallas, TX 75390-9041, United States. mlehrm@mednet.swmed.edu

SO Molecular Biology of the Cell, (2001) Vol. 12, No. 2, pp. 487-501. .
Refs: 47
ISSN: 1059-1524 CODEN: MBCEEV

CY United States

DT Journal; Article

FS 022 Human Genetics
029 Clinical Biochemistry

LA English

SL English

ED Entered STN: 30 Nov 2001
Last Updated on STN: 30 Nov 2001

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CT Medical Descriptors:
*gene isolation
*carbohydrate analysis
*enzyme analysis
*enzyme mechanism
protein folding
hamster
phenotype
endoplasmic reticulum
gene mutation
amino acid sequence
catalysis
fluorescence in situ hybridization
mammal
nonhuman

animal cell
article
priority journal
Drug Descriptors:
*gene product: EC, endogenous compound
*protein lec 35: EC, endogenous compound
*monosaccharide: EC, endogenous compound
*dolichol: EC, endogenous compound
*glycosyltransferase: EC, endogenous compound
complementary DNA: EC, endogenous compound
mutant protein: EC, endogenous compound
membrane protein: EC, endogenous compound
unclassified drug
RN (dolichol) 11029-02-0; (glycosyltransferase) 9033-07-2

animal cell
article
priority journal
Drug Descriptors:
*gene product: EC, endogenous compound
*protein lec 35: EC, endogenous compound
*monosaccharide: EC, endogenous compound
*dolichol: EC, endogenous compound
*glycosyltransferase: EC, endogenous compound
complementary DNA: EC, endogenous compound
mutant protein: EC, endogenous compound
membrane protein: EC, endogenous compound
unclassified drug
RN (dolichol) 11029-02-0; (glycosyltransferase) 9033-07-2

ANSWER 3 OF 3 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN

AN 97072518 EMBASE

DN 1997072518

TI Further studies in α- C-mannosylation promoted by samarium diiodide.

AU Jarreton O.; Skrydstrup T.; Beau J.-M.

CS T. Skrydstrup, Laboratoire de Synthese Biomolecules, Associe au CNRS, Univ. de Paris-Sud, Associe au CNRS, F-91405 Orsay, France. skryds@icmo.u-psud.fr

SO Tetrahedron Letters, (1997) Vol. 38, No. 10, pp. 1767-1770. .
Refs: 11
ISSN: 0040-4039 CODEN: TELEAY

PUI S 0040-4039(97)00206-2

CY United Kingdom

DT Journal; Article

FS 037 Drug Literature Index

LA English

SL English

ED Entered STN: 24 Mar 1997
Last Updated on STN: 24 Mar 1997

AB Mannosyl pyridylsulfones with varying C2-OH protecting groups were reacted with cyclohexanone in the presence of SmI2. With SiMe2tBu and Bn, high yields of an α-C-mannoside were obtained, In the former case no β-elimination was observed. The relative configuration of the major diastereomer obtained upon coupling with aldehydes was determined.

CT Medical Descriptors:
*carbohydrate synthesis
article
conformational transition
glycosylation
nuclear magnetic resonance spectroscopy
stereochemistry
stereoisomerism
Drug Descriptors:
*mannoside: AN, drug analysis
*mannoside: DV, drug development
cyclohexanone
samarium

RN (mannoside) 50986-23-7; (cyclohexanone) 108-94-1; (samarium) 7440-19-9

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10/530,457
Look Search
5/11/07

d his

(FILE 'HOME' ENTERED AT 16:29:45 ON 11 MAY 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 16:29:59 ON 11 MAY 2007

L1	8	S	(C MANNOSYLTRANSFERASE?)
L2	20778	S	(TRANSGENIC ANIMAL)
L3	0	S	L1 AND L2
L4	4	S	L1 AND VIVO?
L5	1	DUPLICATE REMOVE	L4 (3 DUPLICATES REMOVED)
L6	144	S	(C MANNOSYL?)
L7	7	S	L6 AND VIVO
L8	2	DUPLICATE REMOVE	L7 (5 DUPLICATES REMOVED)
L9	1	S	L8 NOT L5
L10	67	S	(CMT GENE)
L11	0	S	L10 AND VIVO?
L12	24	S	L10 AND ANIMAL?
L13	17	DUPLICATE REMOVE	L12 (7 DUPLICATES REMOVED)
L14	11	S	L13 AND PD<2004
L15	0	S	(TRANSGENTIC ANIMAL)
L16	21382	S	(TRANSGEN? ANIMAL)
L17	12523	S	MANNOSYL?
L18	4	S	L16 AND L17
L19	4	DUPLICATE REMOVE	L18 (0 DUPLICATES REMOVED)
L20	3	S	L19 AND PD<2004

=>

ANSWER 2 OF 3 MEDLINE on STN

AN 2001569366 MEDLINE

DN PubMed ID: 11486004

TI Remodeling of the major pig xenoantigen by N-acetylglucosaminyltransferase III in transgenic pig.

AU Miyagawa S; Murakami H; Takahagi Y; Nakai R; Yamada M; Murase A; Koyota S; Koma M; Matsunami K; Fukuta D; Fujimura T; Shigehisa T; Okabe M; Nagashima H; Shirakura R; Taniguchi N

CS Department of Regenerative Medicine, Osaka University Graduate School of Medicine, the Genome Information Research Center, Osaka University, Suita, Osaka 565-0871, Japan.. miyagawa@orgtrp.med.osaka-u.ac.jp

SO The Journal of biological chemistry, (2001 Oct 19) Vol. 276, No. 42, pp. 39310-9. Electronic Publication: 2001-08-02.
Journal code: 2985121R. ISSN: 0021-9258.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals

EM 200112

ED Entered STN: 29 Oct 2001
Last Updated on STN: 5 Jan 2003
Entered Medline: 4 Dec 2001

AB We have been successful in generating several lines of transgenic mice and pigs that contain the human beta-d-mannoside beta-1,4-N-acetylglucosaminyltransferase III (GnT-III) gene. The overexpression of the GnT-III gene in mice and pigs reduced their antigenicity to human natural antibodies, especially the Galalpha1-3Galbeta1-4GlcNAc-R, as evidenced by immunohistochemical analysis. Endothelial cell studies from the GnT-III transgenic pigs also revealed a significant down-regulation in antigenicity, including Hanganutziu-Deicher antigen, and dramatic reductions in both the complement- and natural killer cell-mediated pig cell lyses. Changes in the enzymatic activities of other glycosyltransferases, such as alpha1,3-galactosyltransferase, GnT-IV, and GnT-V, did not support cross-talk between GnT-III and these enzymes in the transgenic animals. In addition, we demonstrated the effect of GnT-III in down-regulating the xenoantigen of pig heart grafts, using a pig to cynomolgus monkey transplantation model, suggesting that this approach may be useful in clinical xenotransplantation in the future.

CT Check Tags: Female; Male
Animals
Animals, Genetically Modified
*Antigens, Heterophile: CH, chemistry
*Antigens, Heterophile: GE, genetics
Cell Line
Down-Regulation
Flow Cytometry
Glycosyltransferases: ME, metabolism
Heart Transplantation
Humans
Immunohistochemistry
L-Lactate Dehydrogenase: ME, metabolism
Macaca fascicularis
Mice
*N-Acetylglucosaminyltransferases: ME, metabolism
Promoter Regions (Genetics)
Swine
Tissue Distribution
Transplantation, Heterologous

CN 0 (Antigens, Heterophile); EC 1.1.1.27 (L-Lactate Dehydrogenase); EC 2.4.-(Glycosyltransferases); EC 2.4.1.- (N-Acetylglucosaminyltransferases); EC 2.4.1.144 (beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase)

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     (FILE 'HOME' ENTERED AT 16:29:45 ON 11 MAY 2007)

     FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 16:29:59 ON 11
     MAY 2007
L1             8 S (C MANNOSYLTRANSFERASE?)
L2         20778 S (TRANSGENIC ANIMAL)
L3             0 S L1 AND L2
L4             4 S L1 AND VIVO?
L5             1 DUPLICATE REMOVE L4 (3 DUPLICATES REMOVED)
L6           144 S (C MANNOSYL?)
L7             7 S L6 AND VIVO
L8             2 DUPLICATE REMOVE L7 (5 DUPLICATES REMOVED)
L9             1 S L8 NOT L5
L10           67 S (CMT GENE)
L11            0 S L10 AND VIVO?
L12           24 S L10 AND ANIMAL?
L13           17 DUPLICATE REMOVE L12 (7 DUPLICATES REMOVED)
L14           11 S L13 AND PD<2004
L15            0 S (TRANSGENTIC ANIMAL)
L16        21382 S (TRANSGEN? ANIMAL)
L17        12523 S MANNOSYL?
L18            4 S L16 AND L17
L19            4 DUPLICATE REMOVE L18 (0 DUPLICATES REMOVED)
L20            3 S L19 AND PD<2004

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Search.

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     (FILE 'HOME' ENTERED AT 14:22:42 ON 11 MAY 2007)

     FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 14:22:59 ON 11
     MAY 2007
L1            43 S (C MANNOSYLATE?)
L2             4 S L1 AND PROTEASE?
L3            42 S L1 AND PROTEIN?
L4        186739 S (FUSION PROTEIN)
L5             1 S L4 AND L1
L6             0 S L5 AND L2
L7             1 DUPLICATE REMOVE L2 (3 DUPLICATES REMOVED)

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